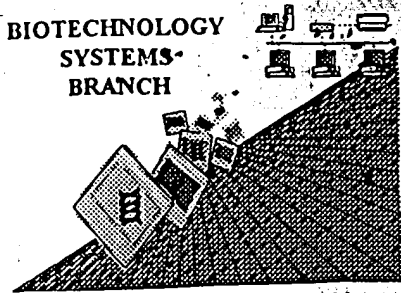BIOTECHNOLOGY
SYSTEMS·
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____09/991900_____

Source: _____OIPE_____

Date Processed by STIC: _____11/08/01_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/581900_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1____ Wrapped Nucleics / Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length

Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequen<
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/981,900

DATE: 11/08/2001
TIME: 13:18:37

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11082001\I981900.raw**

```
   3 <110> APPLICANT: Sticklen, Masomeh B
   4        Maqbool, Shahina B
   5        Dale, Bruce E
   7 <120> TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
DEGRADE LIGNIN
   8        AND CELLULOSE TO FERMENTABLE SUGARS
  10 <130> FILE REFERENCE: MSU 4.1-539
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/981,900
C--> 12 <141> CURRENT FILING DATE: 2001-10-18
  12 <150> PRIOR APPLICATION NUMBER: 60/242,408
  13 <151> PRIOR FILING DATE: 2000-10-20
  15 <160> NUMBER OF SEQ ID NOS: 22
  17 <170> SOFTWARE: PatentIn version 3.1
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 1110
  21 <212> TYPE: DNA
  22 <213> ORGANISM: Oryza sativa
  24 <400> SEQUENCE: 1
  25 gggtcggaga tgccaccacg gccacaaccc acgagcccgg cgcgacacca ccgcgcgcgt      60
  27 tgagccagcc acaaacgccc gcggataggc gcgccgcacg cggccaatcc taccacatcc     120
  29 ccggcctccg cggctcgagc gccgtgccat ccgatccgct gagttttggc tatttatacg     180
  31 taccgcggga gcctgtgtgc agagagtgca tctcaagaag tactcgagca aagaaggaga     240
  33 gagcttggtg agctgcagag atggcccccct ccgtgatggc gtcgtcggcc accaccgtcg     300
  35 ctcccttcca gggctcaagt ccaccgccgg catgccgtcg cccgccgtcc gaactccagc     360
  37 ttcggcaacg tcagcatggc ggcaggatca ggtgcatgca ggtaattacc tactgatcca     420
  39 acacacattc ttcttcttct tcttcttctt aaccaacatt aaccaacaac tcaattatcg     480
  41 tttattcatt gaggtgtggc cgattgaggg catcaagaag ttcgagaccc tctcctacct     540
  43 gccaccgctc accgtggagg acctcctgaa gcagatcgag tacctagctc cgttccaagt     600
  45 ggtgccctgc ctcgagttca gcaaggtcgg atttgtctac cgtgagaacc acaagtcccc     660
  47 tggatactac gacggcaggt actggaccat gtggaagctg cccatgttcg ggtgcaccga     720
  49 cgccacccag gtcgtcaagg agctcgagga ggccaagaag gcgtaccctg atgcattcgt     780
  51 ccgtatcatc ggcttcgaca cgttaggca ggtgcagctc atcagcttca tcgcctacaa     840
  53 cccgggctgc gaggagtctg gtggcaacta agccgtcatc gtcatatata gcctcgttta     900
  55 attgttcatc tctgattcga tgatgtctcc caccttgttt cgtgtgttcc cagtttgttt     960
  57 catcgtcttt tgattttacc ggccgtgctc tgctttttgtt ttttctttttc acctgattct    1020
  59 ctctctgact tgatgtaaga gtggtatctg ctacgactat atgttgtttg ggtgaggcat    1080
  61 atgtgaatga aatctatgaa agctccggct                                     1110
  64 <210> SEQ ID NO: 2
  65 <211> LENGTH: 38
  66 <212> TYPE: PRT
  67 <213> ORGANISM: Oryza sativa
  69 <400> SEQUENCE: 2
  71 Met Ala Pro Ser Val Met Ala Ser Ser Ala Thr Thr Val Ala Pro Phe
  72 1               5                   10                  15
  75 Gln Gly Ser Ser Pro Pro Pro Ala Cys Arg Arg Pro Pro Ser Glu Leu
  76             20                  25                  30
  79 Gln Leu Arg Gln Arg Gln
  80         35
```

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 11/08/2001
PATENT APPLICATION: US/09/981,900   TIME: 13:18:37

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11082001\I981900.raw**

```
 83 <210> SEQ ID NO: 3
 84 <211> LENGTH: 6
 85 <212> TYPE: PRT
 86 <213> ORGANISM: synthetic peptide
 88 <220> FEATURE:
 89 <221> NAME/KEY: SIGNAL
 90 <222> LOCATION: (1)..(6)
 91 <223> OTHER INFORMATION: targets the peroxisomes of plants
 94 <400> SEQUENCE: 3
 96 Arg Ala Val Ala Arg Leu
 97 1               5
100 <210> SEQ ID NO: 4
101 <211> LENGTH: 3004
102 <212> TYPE: DNA
103 <213> ORGANISM: Acidothermus cellulolyticus
105 <220> FEATURE:
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (824)..(2512)
108 <223> OTHER INFORMATION: E I beta-1,4-endoglucanase precursor
111 <400> SEQUENCE: 4
112 ggatccacgt tgtacaaggt cacctgtccg tcgttctggt agagcggcgg gatggtcacc       60
114 cgcacgatct ctcctttgtt gatgtcgacg gtcacgtggt tacggtttgc ctcggccgcg      120
116 attttcgcgc tcgggcttgc tccggctgtc gggttcggtt ggcgtggtg tgcggagcac      180
118 gccgaggcga tcccaatgag ggcaagggca agagcggagc cgatggcacg tcgggtggcc      240
120 gatggggtac gccgatgggg cgtggcgtcc ccgccgcgga cagaaccgga tgcggaatag      300
122 gtcacggtgc gacatgttgc cgtaccgcgg acccggatga caagggtggg tgcgcgggtc      360
124 gcctgtgagc tgccggctgg cgtctggatc atgggaacga tcccaccatt ccccgcaatc      420
126 gacgcgatcg ggagcagggc ggcgcgagcc ggaccgtgtg gtcgagccgg acgattcgcc      480
128 catacggtgc tgcaatgccc agcgccatgt tgtcaatccg ccaaatgcag caatgcacac      540
130 atggacaggg attgtgactc tgagtaatga ttggattgcc ttcttgccgc ctacgcgtta      600
132 cgcagagtag gcgactgtat gcggtaggtt ggcgctccag ccgtgggctg gacatgcctg      660
134 ctgcgaactc ttgacacgtc tggttgaacg cgcaatactc ccaacaccga tgggatcgtt      720
136 cccataagtt tccgtctcac aacagaatcg gtgcgccctc atgatcaacg tgaaaggagt      780
138 acgggggaga acagacgggg gagaaaccaa cgggggattg gcg gtg ccg cgc gca      835
139                                                 Val Pro Arg Ala
140                                                 1
142 ttg cgg cga gtg cct ggc tcg cgg gtg atg ctg cgg gtc ggc gtc gtc      883
143 Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg Val Gly Val Val
144 5               10                  15                  20
146 gtc gcg gtg ctg gca ttg gtt gcc gca ctc gcc aac cta gcc gtg ccg      931
147 Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn Leu Ala Val Pro
148             25                  30                  35
150 cgg ccg gct cgc gcc gcg ggc ggc ggc tat tgg cac acg agc ggc cgg      979
151 Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His Thr Ser Gly Arg
152             40                  45                  50
154 gag atc ctg gac gcg aac aac gtg ccg gta cgg atc gcc ggc atc aac     1027
155 Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn
156             55                  60                  65
158 tgg ttt ggg ttc gaa acc tgc aat tac gtc gtg cac ggt ctc tgg tca     1075
```

[Handwritten annotation, partially legible:] "Errored. Synthetic peptide is not a valid 213 response. "Artificial Sequence", "Unknown" or the name of some particular species are the only appropriate responses."

```
159 Trp Phe Gly Phe Glu Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser
160     70              75              80
162 cgc gac tac cgc agc atg ctc gac cag ata aag tcg ctc ggc tac aac      1123
163 Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn
164 85              90              95              100
166 aca atc cgg ctg ccg tac tct gac gac att ctc aag ccg ggc acc atg      1171
167 Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met
168             105             110             115
170 ccg aac agc atc aat ttt tac cag atg aat cag gac ctg cag ggt ctg      1219
171 Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu
172             120             125             130
174 acg tcc ttg cag gtc atg gac aaa atc gtc gcg tac gcc ggt cag atc      1267
175 Thr Ser Leu Gln Val Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile
176         135             140             145
178 ggc ctg cgc atc att ctt gac cgc cac cga ccg gat tgc agc ggg cag      1315
179 Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln
180     150             155             160
182 tcg gcg ctg tgg tac acg agc agc gtc tcg gag gct acg tgg att tcc      1363
183 Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser
184 165             170             175             180
186 gac ctg caa gcg ctg gcg cag cgc tac aag gga aac ccg acg gtc gtc      1411
187 Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val
188             185             190             195
190 ggc ttt gac ttg cac aac gag ccg cat gac ccg gcc tgc tgg ggc tgc      1459
191 Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys
192             200             205             210
194 ggc gat ccg agc atc gac tgg cga ttg gcc gcc gag cgg gcc gga aac      1507
195 Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn
196         215             220             225
198 gcc gtg ctc tcg gtg aat ccg aac ctg ctc att ttc gtc gaa ggt gtg      1555
199 Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val
200     230             235             240
202 cag agc tac aac gga gac tcc tac tgg tgg ggc ggc aac ctg caa gga      1603
203 Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly
204 245             250             255             260
206 gcc ggc cag tac ccg gtc gtg ctg aac gtg ccg aac cgc ctg gtg tac      1651
207 Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr
208             265             270             275
210 tcg gcg cac gac tac gcg acg agc gtc tac ccg cag acg tgg ttc agc      1699
211 Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser
212             280             285             290
214 gat ccg acc ttc ccc aac aac atg ccc ggc atc tgg aac aag aac tgg      1747
215 Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp
216         295             300             305
218 gga tac ctc ttc aat cag aac att gca ccg gta tgg ctg ggc gaa ttc      1795
219 Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe
220     310             315             320
222 ggt acg aca ctg caa tcc acg acc gac cag acg tgg ctg aag acg ctc      1843
223 Gly Thr Thr Leu Gln Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu
```

RAW SEQUENCE LISTING   DATE: 11/08/2001
PATENT APPLICATION: US/09/981,900   TIME: 13:18:37

Input Set : A:\es.txt
Output Set: N:\CRF3\11082001\I981900.raw

```
224 325              330              335              340
226 gtc cag tac cta cgg ccg acc gcg caa tac ggt gcg gac agc ttc cag    1891
227 Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln
228              345              350              355
230 tgg acc ttc tgg tcc tgg aac ccc gat tcc ggc gac aca gga gga att    1939
231 Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile
232              360              365              370
234 ctc aag gat gac tgg cag acg gtc gac aca gta aaa gac ggc tat ctc    1987
235 Leu Lys Asp Asp Trp Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu
236          375              380              385
238 gcg ccg atc aag tcg tcg att ttc gat cct gtc ggc gcg tct gca tcg    2035
239 Ala Pro Ile Lys Ser Ser Ile Phe Asp Pro Val Gly Ala Ser Ala Ser
240      390              395              400
242 cct agc agt caa ccg tcc ccg tcg gtg tcg ccg tct ccg tcg ccg agc    2083
243 Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser Pro Ser Pro Ser
244 405              410              415              420
246 ccg tcg gcg agt cgg acg ccg acg cct act ccg acg ccg aca gcc agc    2131
247 Pro Ser Ala Ser Arg Thr Pro Thr Pro Thr Pro Thr Pro Thr Ala Ser
248              425              430              435
250 ccg acg cca acg ctg acc cct act gct acg ccc acg ccc acg gca agc    2179
251 Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr Pro Thr Ala Ser
252              440              445              450
254 ccg acg ccg tca ccg acg gca gcc tcc gga gcc cgc tgc acc gcg agt    2227
255 Pro Thr Pro Ser Pro Thr Ala Ala Ser Gly Ala Arg Cys Thr Ala Ser
256          455              460              465
258 tac cag gtc aac agc gat tgg ggc aat ggc ttc acg gta acg gtg gcc    2275
259 Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr Val Thr Val Ala
260      470              475              480
262 gtg aca aat tcc gga tcc gtc gcg acc aag aca tgg acg gtc agt tgg    2323
263 Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp Thr Val Ser Trp
264 485              490              495              500
266 aca ttc ggc gga aat cag acg att acc aat tcg tgg aat gca gcg gtc    2371
267 Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val
268              505              510              515
270 acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac    2419
271 Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn
272              520              525              530
274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat    2467
275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr
276          535              540              545
278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa        2512
279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser
280      550              555              560
282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag  2572
284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgcc  2632
286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc  2692
288 gtgccgctgg cgatgcagca tcctgccatc gccgcgacgc acgtcgacaa tccctatgcg  2752
290 ggagcgacct tcttcgtcaa cccgtactgg gcgcaagaag tacagagcga acggcgaacc  2812
292 agaccaatgc cactctcgca gcgaaaatgc gcgtcgtttc cacatattcg acggccgtct  2872
```

RAW SEQUENCE LISTING   DATE: 11/08/2001
PATENT APPLICATION: US/09/981,900   TIME: 13:18:37

Input Set : A:\es.txt
Output Set: N:\CRF3\11082001\I981900.raw

```
294 ggatggaccg catcgctgcg atcaacggcg tcaacggcgg acccggcttg acgacatatc   2932
296 tggacgccgc cctctcccag cagcagggaa ccaccccctga agtcattgag attgtcatct   2992
298 acgatctgcc gg                                                        3004
301 <210> SEQ ID NO: 5
302 <211> LENGTH: 562
303 <212> TYPE: PRT
304 <213> ORGANISM: Acidothermus cellulolyticus
306 <400> SEQUENCE: 5
308 Val Pro Arg Ala Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg
309 1               5                   10                  15
312 Val Gly Val Val Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn
313             20                  25                  30
316 Leu Ala Val Pro Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His
317         35                  40                  45
320 Thr Ser Gly Arg Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile
321     50                  55                  60
324 Ala Gly Ile Asn Trp Phe Gly Phe Glu Thr Cys Asn Tyr Val Val His
325 65                  70                  75                  80
328 Gly Leu Trp Ser Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser
329             85                  90                  95
332 Leu Gly Tyr Asn Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys
333             100                 105                 110
336 Pro Gly Thr Met Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp
337         115                 120                 125
340 Leu Gln Gly Leu Thr Ser Leu Gln Val Met Asp Lys Ile Val Ala Tyr
341     130                 135                 140
344 Ala Gly Gln Ile Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp
345 145                 150                 155                 160
348 Cys Ser Gly Gln Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala
349             165                 170                 175
352 Thr Trp Ile Ser Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn
353             180                 185                 190
356 Pro Thr Val Val Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala
357         195                 200                 205
360 Cys Trp Gly Cys Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu
361     210                 215                 220
364 Arg Ala Gly Asn Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe
365 225                 230                 235                 240
368 Val Glu Gly Val Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly
369             245                 250                 255
372 Asn Leu Gln Gly Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn
373             260                 265                 270
376 Arg Leu Val Tyr Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln
377         275                 280                 285
380 Thr Trp Phe Ser Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp
381     290                 295                 300
384 Asn Lys Asn Trp Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp
385 305                 310                 315                 320
388 Leu Gly Glu Phe Gly Thr Thr Leu Gln Ser Thr Thr Asp Gln Thr Trp
```

11/8/01

VERIFICATION SUMMARY   DATE: 11/08/2001
PATENT APPLICATION: US/09/981,900   TIME: 13:18:38

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11082001\I981900.raw**

```
L:12  M:270 C: Current Application Number differs, Replaced Current Application No
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
```